

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/527,195
Source: PCR
Date Processed by STIC: 1/31/06

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 01/31/2006

PATENT APPLICATION: US/10/527,195

TIME: 15:54:33

Input Set : A:\10527195.txt

Output Set: N:\CRF4\01312006\J527195.raw

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3 <110> APPLICANT: Yasufumi KANEDA
4   Kazuo OSHIMA
5   Ryuichi MORISHITA
6   Takeshi KUBO
7   AnGes MG, Inc.
9 <120> TITLE OF INVENTION: Pharmaceutical Preparation for Hearing Impairment
11 <130> FILE REFERENCE: 423-69 / 03059PCT
13 <140> CURRENT APPLICATION NUMBER: US 10/527,195
14 <141> CURRENT FILING DATE: 2005-03-10
16 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/012674
17 <151> PRIOR FILING DATE: 2003-10-02
19 <150> PRIOR APPLICATION NUMBER: JP 2002-289639
20 <151> PRIOR FILING DATE: 2002-10-02
22 <160> NUMBER OF SEQ ID NOS: 6
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 728
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
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31 Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu
32   1               5               10               15
34 Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
35               20               25               30
37 Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
38               35               40               45
40 Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val
41   50               55               60
43 Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
44 65               70               75               80
46 Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
47               85               90               95
49 Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
50               100              105              110
52 Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys
53               115              120              125
55 Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys
56               130              135              140
58 Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His
59 145              150              155              160
61 Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr
62               165              170              175
64 Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser

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65          180          185          190
67 Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu
68          195          200          205
70 Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp
71          210          215          220
73 His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro
74 225          230          235          240
76 His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp
77          245          250          255
79 Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr
80          260          265          270
82 Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys
83          275          280          285
85 Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu
86          290          295          300
88 Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile
89 305          310          315          320
91 Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu
92          325          330          335
94 His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn
95          340          345          350
97 Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr
98          355          360          365
100 Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp
101          370          375          380
103 Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met
104 385          390          395          400
106 Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp
107          405          410          415
109 Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala
110          420          425          430
112 Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His
113          435          440          445
115 Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys
116          450          455          460
118 Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu
119 465          470          475          480
121 Asp His Pro Val Ile Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val
122          485          490          495
124 Asn Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg
125          500          505          510
127 Tyr Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp
128          515          520          525
130 Val Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr
131          530          535          540
133 Glu Ala Trp Leu Gly Ile His Asp Val His Gly Arg Gly Asp Glu Lys
134 545          550          555          560
136 Cys Lys Gln Val Leu Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly
137          565          570          575

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139 Ser Asp Leu Val Leu Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp
140                               580                               585                               590
142 Phe Val Ser Thr Ile Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu
143                               595                               600                               605
145 Lys Thr Ser Cys Ser Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn
146                               610                               615                               620
148 Tyr Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu
149 625                               630                               635                               640
151 Lys Cys Ser Gln His His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu
152                               645                               650                               655
154 Ile Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp
155                               660                               665                               670
157 Tyr Gly Gly Pro Leu Val Cys Glu Gln His Lys Met Arg Met Val Leu
158                               675                               680                               685
160 Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly
161                               690                               695                               700
163 Ile Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile
164 705                               710                               715                               720
166 Leu Thr Tyr Lys Val Pro Gln Ser
167                               725

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169 <210> SEQ ID NO: 2

170 <211> LENGTH: 2187

171 <212> TYPE: DNA

172 <213> ORGANISM: Homo sapiens

W--> 173 <400> SEQUENCE: 2

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174 atgtgggtga ccaaaactcct gccagccctg ctgctgcagc atgtcctcct gcatctcctc 60
175 ctgctcccca tcgccatccc ctatgcagag ggacaaaagga aaagaagaaa tacaattcat 120
176 gaattcaaaa aatcagcaaaa gactacccta atcaaaaatag atccagcact gaagataaaa 180
177 accaaaaaag tgaataactgc agaccaatgt gctaatagat gtactaggaa taaaggactt 240
178 ccattcactt gcaaggcttt tgtttttgat aaagcaagaa aacaatgcct ctgggtcccc 300
179 ttcaatagca tgtcaagtgg agtgaaaaaa gaatttggcc atgaatttga cctctatgaa 360
180 aacaaagact acattagaaa ctgcatcatt ggtaaaggac gcagctacaa gggaacagta 420
181 tctatcacta agagtggcat caaatgtcag ccctggagtt ccatgatacc acacgaacac 480
182 agctttttgc cttcgagcta tcgggggtaaa gacctacagg aaaactactg tcgaaatcct 540
183 cgagggggaag aaggggggacc ctggtgtttc acaagcaatc cagaggtacg ctacgaagtc 600
184 tgtgacattc ctcagtgttc agaagttgaa tgcattgacct gcaatgggga gagttatcga 660
185 ggtctcatgg atcatacaga atcaggcaag atttgtcagc gctgggatca tcagacacca 720
186 caccggcaca aattcttgcc tgaaagatat cccgacaagg gctttgatga taattattgc 780
187 cgcaatcccg atggccagcc gagggccatg tgctatactc ttgacctca caccgctgg 840
188 gagtactgtg caattaaaac atgcgctgac aatactatga atgacactga tgttcctttg 900
189 gaaacaactg aatgcattcca aggtcaagga gaaggctaca ggggcactgt caataccatt 960
190 tgggaatggaa ttccatgtca gcgttgggat tctcagtatc ctcacgagca tgacatgact 1020
191 cctgaaaatt tcaagtgcaa ggacctacga gaaaattact gccgaaatcc agatgggtct 1080
192 gaatcaccct ggtgttttac cactgatcca aacatccgag ttggctactg ctcccaaatt 1140
193 ccaaactgtg atatgtcaca tggacaagat tgttatcgtg ggaatggcaa aaattatatg 1200
194 ggcaacttat cccaaacaag atctggacta acatgttcaa tgtgggacaa gaacatggaa 1260
195 gacttacatc gtcatatctt ctgggaacca gatgcaagta agctgaatga gaattactgc 1320
196 cgaaatccag atgatgatgc tcatggaccc tgggtgctaca cgggaaatcc actcattcct 1380
197 tgggattatt gccctatttc tcgttgtgaa ggtgatacca cacctacaat agtcaattta 1440

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198 gaccatcccg taatatcttg tgccaaaacg aaacaattgc gagttgtaaa tgggattcca 1500
199 acacgaacaa acataggatg gatggtagt ttgagataca gaaataaaca tatctgcgga 1560
200 ggatcattga taaaggagag ttgggttctt actgcacgac agtgtttccc ttctcgagac 1620
201 ttgaaagatt atgaagcttg gcttggaatt catgatgtcc acggaagagg agatgagaaa 1680
202 tgcaaacagg ttctcaatgt ttcccagctg gtatatggcc ctgaaggatc agatctgggt 1740
203 ttaatgaagc ttgccaggcc tgctgtcctg gatgattttg ttagtacgat tgatttacct 1800
204 aattatggat gcacaattcc tgaaaagacc agttgcagtg tttatggctg gggctacact 1860
205 ggattgatca actatgatgg cctattacga gtggcacatc tctatataat gggaaatgag 1920
206 aaatgcagcc agcatcatcg agggaagggt actctgaatg agtctgaaat atgtgctggg 1980
207 gctgaaaaga ttggatcagg accatgtgag ggggattatg gtggccact tgtttgtgag 2040
208 caacataaaa tgagaatggg tcttggtgtc attgttcctg gtcgtggatg tgccattcca 2100
209 aatcgtcctg gtatttttgt ccgagtagca tattatgcaa aatggataca caaaattatt 2160
210 ttaacatata aggtaccaca gtcatag 2187

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212 <210> SEQ ID NO: 3

213 <211> LENGTH: 24

214 <212> TYPE: DNA

215 <213> ORGANISM: Artificial Sequence

217 <220> FEATURE:

218 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

220 <400> SEQUENCE: 3

C--> 221 ttcacaagca atccagaggt acgc 24

223 <210> SEQ ID NO: 4

224 <211> LENGTH: 24

225 <212> TYPE: DNA

226 <213> ORGANISM: Artificial Sequence

228 <220> FEATURE:

229 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

231 <400> SEQUENCE: 4

C--> 232 gaggtcaag agtatagcac catg 24

234 <210> SEQ ID NO: 5

235 <211> LENGTH: 20

236 <212> TYPE: DNA

237 <213> ORGANISM: Artificial Sequence

239 <220> FEATURE:

240 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

W--> 241 <400> SEQUENCE: 5

C--> 242 tgaaggctcg agtcaacgga 20

244 <210> SEQ ID NO: 6

245 <211> LENGTH: 20

246 <212> TYPE: DNA

247 <213> ORGANISM: Artificial Sequence

249 <220> FEATURE:

250 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

252 <400> SEQUENCE: 6

C--> 253 gatggcatgg actgtggtca 20

VERIFICATION SUMMARY

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Input Set : A:\10527195.txt

Output Set: N:\CRF4\01312006\J527195.raw

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L:173 M:283 W: Missing Blank Line separator, <400> field identifier
L:221 M:112 C: (48) String data converted to lower case,
L:232 M:112 C: (48) String data converted to lower case,
L:241 M:283 W: Missing Blank Line separator, <400> field identifier
L:242 M:112 C: (48) String data converted to lower case,
L:253 M:112 C: (48) String data converted to lower case,